

**RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/530,542  
Source: PCT  
Date Processed by STIC: 11/21/2005

***ENTERED***



PCT

## RAW SEQUENCE LISTING

DATE: 11/21/2005

PATENT APPLICATION: US/10/530,542

TIME: 15:49:29

Input Set : A:\1-32724 SEQLIST.TXT

Output Set: N:\CRF4\11212005\J530542.raw

4 <110> APPLICANT: BAGUTTI; Claudia  
 5 CHIQUET-EHRISMANN; Ruth  
 6 DRABIKOWSKI; Krzysztof; Piotr  
 7 RUBIN-LUCHT; Beatrix; Paulette  
 9 <120> TITLE OF INVENTION: METHODS FOR DETECTING TENEURIN  
 10 SIGNALLING AND RELATED SCREENING METHODS  
 13 <130> FILE REFERENCE: 1-32724A/FMI  
 15 <140> CURRENT APPLICATION NUMBER: 10/530,542  
 C--> 16 <141> CURRENT FILING DATE: 2005-04-07  
 18 <150> PRIOR APPLICATION NUMBER: PCT/EP03/011382  
 19 <151> PRIOR FILING DATE: 2003-10-14  
 21 <150> PRIOR APPLICATION NUMBER: GB0223984  
 22 <151> PRIOR FILING DATE: 2002-10-15  
 24 <160> NUMBER OF SEQ ID NOS: 20  
 26 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
 28 <210> SEQ ID NO: 1  
 29 <211> LENGTH: 963  
 30 <212> TYPE: DNA  
 31 <213> ORGANISM: Homo sapiens  
 33 <220> FEATURE:  
 34 <221> NAME/KEY: CDS  
 35 <222> LOCATION: (1)...(963)  
 36 <223> OTHER INFORMATION: Human teneurin  
 38 <400> SEQUENCE: 1  
 39 atg gag caa act gac tgc aaa ccc tac cag cct cta cca aaa gtc aag 48  
 40 Met Glu Gln Thr Asp Cys Lys Pro Tyr Gln Pro Leu Pro Lys Val Lys  
 41 1 5 10 15  
 43 cat gaa atg gat cta gct tac acc agt tct tct gat gag agt gaa gat 96  
 44 His Glu Met Asp Leu Ala Tyr Thr Ser Ser Ser Asp Glu Ser Glu Asp  
 45 20 25 30  
 47 gga aga aaa cca aga cag tca tac aac tcc agg gag acc ctg cac gag 144  
 48 Gly Arg Lys Pro Arg Gln Ser Tyr Asn Ser Arg Glu Thr Leu His Glu  
 49 35 40 45  
 51 tat aac cag gag ctg agg atg aat tac aat agc cag agt aga aag agg 192  
 52 Tyr Asn Gln Glu Leu Arg Met Asn Tyr Asn Ser Gln Ser Arg Lys Arg  
 53 50 55 60  
 55 aaa gaa gta gaa aaa tct act caa gag atg gaa ttc tgt gaa acc tct 240  
 56 Lys Glu Val Glu Lys Ser Thr Gln Glu Met Glu Phe Cys Glu Thr Ser  
 57 65 70 75 80  
 59 cac act ctg tgc tct ggc tac caa aca gac atg cac agc gtt tct cgg 288  
 60 His Thr Leu Cys Ser Gly Tyr Gln Thr Asp Met His Ser Val Ser Arg  
 61 85 90 95  
 63 cat ggc tac cag cta gag atg gga tct gat gtg gac aca gag aca gaa 336

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```

64 His Gly Tyr Gln Leu Glu Met Gly Ser Asp Val Asp Thr Glu Thr Glu
65          100          105          110
67 ggt gct gcc tca cct gac cat gca cta aga atg tgg ata agg gga atg 384
68 Gly Ala Ala Ser Pro Asp His Ala Leu Arg Met Trp Ile Arg Gly Met
69          115          120          125
71 aaa tca gag cat agt tcc tgt ttg tcc agc cgg gcc aac tct gca tta 432
72 Lys Ser Glu His Ser Ser Cys Leu Ser Ser Arg Ala Asn Ser Ala Leu
73          130          135          140
75 tcc ttg act gac act gac cat gaa agg aag tct gat ggg gaa aat gat 480
76 Ser Leu Thr Asp Thr Asp His Glu Arg Lys Ser Asp Gly Glu Asn Asp
77 145          150          155          160
79 gtg cag agc agc cca cac aac cag ttc acc ttc aga ccc ctc cca ccg 528
80 Val Gln Ser Ser Pro His Asn Gln Phe Thr Phe Arg Pro Leu Pro Pro
81          165          170          175
83 cca cct ccg cct cct cat gcc tgc acc tgt gcc agg aag cca ccc cct 576
84 Pro Pro Pro Pro Pro His Ala Cys Thr Cys Ala Arg Lys Pro Pro Pro
85          180          185          190
87 gca gcg gac tct ctt cag agg aga tca atg act acc cgc agc cag ccc 624
88 Ala Ala Asp Ser Leu Gln Arg Arg Ser Met Thr Thr Arg Ser Gln Pro
89          195          200          205
91 agc cca gct gct cca gct ccc cca acc agc acg cag gat tca gtc cat 672
92 Ser Pro Ala Ala Pro Ala Pro Pro Thr Ser Thr Gln Asp Ser Val His
93          210          215          220
95 ctg cat aac agc tgg gtc ctg aac agc aac ata cca ttg gag acc agg 720
96 Leu His Asn Ser Trp Val Leu Asn Ser Asn Ile Pro Leu Glu Thr Arg
97 225          230          235          240
99 cat ttc ctg ttc aaa cat gga tct ggt tcc tct gcg atc ttc agt gca 768
100 His Phe Leu Phe Lys His Gly Ser Gly Ser Ser Ala Ile Phe Ser Ala
101          245          250          255
103 gcc agt cag aac tac cct ctg aca tcc aat acc gtg tac tcg ccc cct 816
104 Ala Ser Gln Asn Tyr Pro Leu Thr Ser Asn Thr Val Tyr Ser Pro Pro
105          260          265          270
107 ccc agg cct ctt cct cga agc acc ttt tcc cga cct gcc ttt acc ttt 864
108 Pro Arg Pro Leu Pro Arg Ser Thr Phe Ser Arg Pro Ala Phe Thr Phe
109          275          280          285
111 aac aaa cct tac agg tgc tgc aac tgg aag tgc aca gca ttg agc gcc 912
112 Asn Lys Pro Tyr Arg Cys Cys Asn Trp Lys Cys Thr Ala Leu Ser Ala
113          290          295          300
115 act gca atc aca gtg act ttg gcc ttg tta cta gcc tat gtg att gca 960
116 Thr Ala Ile Thr Val Thr Leu Ala Leu Leu Leu Ala Tyr Val Ile Ala
117 305          310          315          320
119 gtg 963
120 Val
124 <210> SEQ ID NO: 2
125 <211> LENGTH: 321
126 <212> TYPE: PRT
127 <213> ORGANISM: Homo sapiens
129 <400> SEQUENCE: 2
130 Met Glu Gln Thr Asp Cys Lys Pro Tyr Gln Pro Leu Pro Lys Val Lys

```

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Input Set : A:\1-32724 SEQLIST.TXT

Output Set: N:\CRF4\11212005\J530542.raw

```

131 1          5          10          15
132 His Glu Met Asp Leu Ala Tyr Thr Ser Ser Ser Asp Glu Ser Glu Asp
133          20          25          30
134 Gly Arg Lys Pro Arg Gln Ser Tyr Asn Ser Arg Glu Thr Leu His Glu
135          35          40          45
136 Tyr Asn Gln Glu Leu Arg Met Asn Tyr Asn Ser Gln Ser Arg Lys Arg
137          50          55          60
138 Lys Glu Val Glu Lys Ser Thr Gln Glu Met Glu Phe Cys Glu Thr Ser
139 65          70          75          80
140 His Thr Leu Cys Ser Gly Tyr Gln Thr Asp Met His Ser Val Ser Arg
141          85          90          95
142 His Gly Tyr Gln Leu Glu Met Gly Ser Asp Val Asp Thr Glu Thr Glu
143          100          105          110
144 Gly Ala Ala Ser Pro Asp His Ala Leu Arg Met Trp Ile Arg Gly Met
145          115          120          125
146 Lys Ser Glu His Ser Ser Cys Leu Ser Ser Arg Ala Asn Ser Ala Leu
147          130          135          140
148 Ser Leu Thr Asp Thr Asp His Glu Arg Lys Ser Asp Gly Glu Asn Asp
149 145          150          155          160
150 Val Gln Ser Ser Pro His Asn Gln Phe Thr Phe Arg Pro Leu Pro Pro
151          165          170          175
152 Pro Pro Pro Pro Pro His Ala Cys Thr Cys Ala Arg Lys Pro Pro Pro
153          180          185          190
154 Ala Ala Asp Ser Leu Gln Arg Arg Ser Met Thr Thr Arg Ser Gln Pro
155          195          200          205
156 Ser Pro Ala Ala Pro Ala Pro Pro Thr Ser Thr Gln Asp Ser Val His
157          210          215          220
158 Leu His Asn Ser Trp Val Leu Asn Ser Asn Ile Pro Leu Glu Thr Arg
159 225          230          235          240
160 His Phe Leu Phe Lys His Gly Ser Gly Ser Ser Ala Ile Phe Ser Ala
161          245          250          255
162 Ala Ser Gln Asn Tyr Pro Leu Thr Ser Asn Thr Val Tyr Ser Pro Pro
163          260          265          270
164 Pro Arg Pro Leu Pro Arg Ser Thr Phe Ser Arg Pro Ala Phe Thr Phe
165          275          280          285
166 Asn Lys Pro Tyr Arg Cys Cys Asn Trp Lys Cys Thr Ala Leu Ser Ala
167          290          295          300
168 Thr Ala Ile Thr Val Thr Leu Ala Leu Leu Leu Ala Tyr Val Ile Ala
169 305          310          315          320
170 Val

```

174 &lt;210&gt; SEQ ID NO: 3

175 &lt;211&gt; LENGTH: 1194

176 &lt;212&gt; TYPE: DNA

177 &lt;213&gt; ORGANISM: Homo sapiens

179 &lt;220&gt; FEATURE:

180 &lt;221&gt; NAME/KEY: CDS

181 &lt;222&gt; LOCATION: (1)...(1194)

182 &lt;223&gt; OTHER INFORMATION: Human teneurin

184 &lt;400&gt; SEQUENCE: 3

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DATE: 11/21/2005

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TIME: 15:49:29

Input Set : A:\1-32724 SEQLIST.TXT

Output Set: N:\CRF4\11212005\J530542.raw

```

185 atg gat gta aag gac cgg cga cac cgc tct ttg acc aga gga cgc tgt 48
186 Met Asp Val Lys Asp Arg Arg His Arg Ser Leu Thr Arg Gly Arg Cys
187 1 5 10 15
189 ggc aaa gag tgt cgc tac aca agc tcc tct ctg gac agt gag gac tgc 96
190 Gly Lys Glu Cys Arg Tyr Thr Ser Ser Ser Leu Asp Ser Glu Asp Cys
191 20 25 30
193 cgc gtg ccc aca cag aaa tcc tac agc tcc agt gag act ctg aag gcc 144
194 Arg Val Pro Thr Gln Lys Ser Tyr Ser Ser Ser Glu Thr Leu Lys Ala
195 35 40 45
197 tat gac cat gac agc agg atg cac tat gga aac cga gtc aca gac ctc 192
198 Tyr Asp His Asp Ser Arg Met His Tyr Gly Asn Arg Val Thr Asp Leu
199 50 55 60
201 atc cac cgg gag tca gat gag ttt cct aga caa gga acc aac ttc acc 240
202 Ile His Arg Glu Ser Asp Glu Phe Pro Arg Gln Gly Thr Asn Phe Thr
203 65 70 75 80
205 ctt gcc gaa ctg ggc atc tgt gag ccc tcc cca cac cga agc ggc tac 288
206 Leu Ala Glu Leu Gly Ile Cys Glu Pro Ser Pro His Arg Ser Gly Tyr
207 85 90 95
209 tgc tcc gac atg ggg atc ctt cac cag ggc tac tcc ctt agc aca ggg 336
210 Cys Ser Asp Met Gly Ile Leu His Gln Gly Tyr Ser Leu Ser Thr Gly
211 100 105 110
213 tct gac gcc gac tcc gac acc gag gga ggg atg tct cca gaa cac gcc 384
214 Ser Asp Ala Asp Ser Asp Thr Glu Gly Gly Met Ser Pro Glu His Ala
215 115 120 125
217 atc aga ctg tgg ggc aga ggg ata aaa tcc agg cgc agt tcc ggc ctg 432
218 Ile Arg Leu Trp Gly Arg Gly Ile Lys Ser Arg Arg Ser Ser Gly Leu
219 130 135 140
221 tcc agt cgt gaa aac tcg gcc ctt acc ctg act gac tct gac aac gaa 480
222 Ser Ser Arg Glu Asn Ser Ala Leu Thr Leu Thr Asp Ser Asp Asn Glu
223 145 150 155 160
225 aac aaa tca gat gat gag aac gaa agt cgt ccc att cca cct aca tcc 528
226 Asn Lys Ser Asp Asp Glu Asn Glu Ser Arg Pro Ile Pro Pro Thr Ser
227 165 170 175
229 tcg cct agt ctc ctc cca tct gct cag ctg cct agc tcc cat aat cct 576
230 Ser Pro Ser Leu Leu Pro Ser Ala Gln Leu Pro Ser Ser His Asn Pro
231 180 185 190
233 cca cca gtt agc tgc cag atg cca ttg cta gac agc aac acc tcc cat 624
234 Pro Pro Val Ser Cys Gln Met Pro Leu Leu Asp Ser Asn Thr Ser His
235 195 200 205
237 caa atc atg gac acc aac cct gat gag gaa ttc tcc ccc aat tca tac 672
238 Gln Ile Met Asp Thr Asn Pro Asp Glu Glu Phe Ser Pro Asn Ser Tyr
239 210 215 220
241 ctg ctc aga gca tgc tca ggg ccc cag caa gcc tcc agc agt ggc cct 720
242 Leu Leu Arg Ala Cys Ser Gly Pro Gln Gln Ala Ser Ser Ser Gly Pro
243 225 230 235 240
245 ccg aac cac cac agc cag tcg act ctg agg ccc cct ctc cca ccc cct 768
246 Pro Asn His His Ser Gln Ser Thr Leu Arg Pro Pro Leu Pro Pro Pro
247 245 250 255
249 cac aac cac acg ctg tcc cat cac cac tcg tcc gcc aac tcc ctc aac 816

```

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Input Set : A:\1-32724 SEQLIST.TXT

Output Set: N:\CRF4\11212005\J530542.raw

```

250 His Asn His Thr Leu Ser His His His Ser Ser Ala Asn Ser Leu Asn
251                260                265                270
253 agg aac tca ctg acc aat cgg cgg agt cag atc cac gcc ccg gcc cca 864
254 Arg Asn Ser Leu Thr Asn Arg Arg Ser Gln Ile His Ala Pro Ala Pro
255                275                280                285
257 gcg ccc aat gac ctg gcc acc aca cca gag tcc gtt cag ctt cag gac 912
258 Ala Pro Asn Asp Leu Ala Thr Thr Pro Glu Ser Val Gln Leu Gln Asp
259                290                295                300
261 agc tgg gtg cta aac agc aac gtg cca ctg gag acc cgg cac ttc ctc 960
262 Ser Trp Val Leu Asn Ser Asn Val Pro Leu Glu Thr Arg His Phe Leu
263 305                310                315                320
265 ttc aag acc tcc tcg ggg agc aca ccc ttg ttc agc agc tct tcc ccg 1008
266 Phe Lys Thr Ser Ser Gly Ser Thr Pro Leu Phe Ser Ser Ser Ser Pro
267                325                330                335
269 gga tac cct ttg acc tca gga acg gtt tac acg ccc ccg ccc cgc ctg 1056
270 Gly Tyr Pro Leu Thr Ser Gly Thr Val Tyr Thr Pro Pro Pro Arg Leu
271                340                345                350
273 ctg ccc agg aat act ttc tcc agg aag gct ttc aag ctg aag aag ccc 1104
274 Leu Pro Arg Asn Thr Phe Ser Arg Lys Ala Phe Lys Leu Lys Lys Pro
275                355                360                365
277 tcc aaa tac tgc agc tgg aaa tgt gct gcc ctc tcc gcc att gcc gcg 1152
278 Ser Lys Tyr Cys Ser Trp Lys Cys Ala Ala Leu Ser Ala Ile Ala Ala
279                370                375                380
281 gcc ctc ctc ttg gct att ttg ctg gcg tat ttc ata gca atg 1194
282 Ala Leu Leu Leu Ala Ile Leu Leu Ala Tyr Phe Ile Ala Met
283 385                390                395
287 <210> SEQ ID NO: 4
288 <211> LENGTH: 398
289 <212> TYPE: PRT
290 <213> ORGANISM: Homo sapiens
292 <400> SEQUENCE: 4
293 Met Asp Val Lys Asp Arg Arg His Arg Ser Leu Thr Arg Gly Arg Cys
294 1                5                10                15
295 Gly Lys Glu Cys Arg Tyr Thr Ser Ser Ser Leu Asp Ser Glu Asp Cys
296                20                25                30
297 Arg Val Pro Thr Gln Lys Ser Tyr Ser Ser Ser Glu Thr Leu Lys Ala
298                35                40                45
299 Tyr Asp His Asp Ser Arg Met His Tyr Gly Asn Arg Val Thr Asp Leu
300                50                55                60
301 Ile His Arg Glu Ser Asp Glu Phe Pro Arg Gln Gly Thr Asn Phe Thr
302 65                70                75                80
303 Leu Ala Glu Leu Gly Ile Cys Glu Pro Ser Pro His Arg Ser Gly Tyr
304                85                90                95
305 Cys Ser Asp Met Gly Ile Leu His Gln Gly Tyr Ser Leu Ser Thr Gly
306                100                105                110
307 Ser Asp Ala Asp Ser Asp Thr Glu Gly Gly Met Ser Pro Glu His Ala
308                115                120                125
309 Ile Arg Leu Trp Gly Arg Gly Ile Lys Ser Arg Arg Ser Ser Gly Leu
310                130                135                140

```

## VERIFICATION SUMMARY

PATENT APPLICATION: US/10/530,542

DATE: 11/21/2005

TIME: 15:49:30

Input Set : A:\1-32724 SEQLIST.TXT

Output Set: N:\CRF4\11212005\J530542.raw

L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:672 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
L:676 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10  
L:687 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
L:691 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:11  
L:702 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
L:706 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12  
L:717 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
L:721 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:13  
L:732 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
L:736 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:14  
L:747 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
L:752 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:15  
L:763 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
L:768 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:16  
L:779 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
L:784 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:17  
L:795 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
L:800 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:18